

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 12, 2003, 15:00:12 ; Search time 50 Seconds
(without alignments)
1520.847 Million cell updates/sec

Title: US-09-804-472-2

Perfect score: 4177
Sequence: 1 MAASSDPYLPYDGGDNIPL.....DILRIHAQTANQDPASIMFN 791

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:***
2: PIR1:***
3: PIR2:***
4: PIR3:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4026	96.4	820	2	I37240
2	3996	95.7	760	2	S55473
3	3994	95.6	760	2	I58159
4	3273	78.4	760	2	I37242
5	3240	77.6	747	2	S47327
6	3217	77.0	747	2	I48294
7	2100.5	50.3	735	2	T19065
8	1086	26.0	260	2	I37277
9	1020.5	24.4	772	2	T02805
10	1015	24.3	812	2	T39817
11	999.5	23.9	779	2	S50054
12	773	18.5	810	2	T24009
13	751.5	18.0	802	2	S68426
14	750.5	18.0	789	2	S68427
15	725.5	17.4	869	2	S68428
16	724.5	17.3	800	2	T01843
17	709	17.0	667	2	T40727
18	684.5	16.4	764	2	T07608
19	671.5	16.1	780	2	T02939
20	670.5	16.1	775	2	T52107
21	657.5	15.7	902	2	T16821
22	652	15.6	907	2	S23399
23	649	15.5	950	2	T15815
24	646	15.5	822	2	S68210
25	635.5	15.2	887	2	T25358
26	624.5	15.0	880	2	T18771
27	602.5	14.4	994	2	S19595
28	591	14.1	810	2	S19725
29	590.5	14.1	805	2	S13410

30	579.5	13.9	988	2	S37078	chloride channel p
31	534	12.8	687	2	A57713	chloride channel C
32	530.5	12.7	687	2	D57713	chloride channel C
33	530	12.7	687	2	C57713	chloride channel C
34	519.5	12.4	871	2	AC2417	hypothetical prote
35	504.5	12.1	687	2	B57713	hypothetical channel K
36	481.5	11.5	686	2	A45483	chloride channel
37	459	11.0	899	2	S76449	hypothetical prote
38	371.5	8.9	792	2	A84308	chloride channel l
39	370.5	8.9	512	2	H86832	hypothetical prote
40	342.5	8.2	468	2	C82449	conserved hypothet
41	336	8.0	516	2	A95134	voltage-gated chlo
42	336	8.0	521	2	E98002	conserved hypothet
43	314	7.5	586	2	A12065	hypothetical prote
44	304.5	7.3	473	2	AE0527	probable membrane
45	304.5	7.3	589	2	F69426	chloride channel,

ALIGNMENTS

RESULT 1

I37240

Chloride channel protein 3, long form - human

N:Contains: chloride channel protein 3, short form

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence, revision 24-May-1996 #text_change 21-Jul-2000

C/Accession: I37240; I37241; S55475

R:Horstmann, G.; Rugerli, E.; Tagliatela, M.; Wong, C.; Ballabio, A.

A>Title: Characterization of a human and murine gene (CLCN3) sharing similarities to

A:Reference number: A57067; M01D:95394449; PMID:765160

A:Accession: I37240

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-820 <RES>

A:Cross-references: EMBL:X78520; NID:g854101; PIDN:CAA55280.1; PID:g854102

A:Accession: I37241

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 59-820 <RES>

A:Cross-references: EMBL:X78520; NID:g854101; PIDN:CAA55281.1; PID:g854103

C:Genetics:

A:Gene: GDB:CLCN3

A:Cross-references: GDB:270665; OMIM:600580

A:Map position: 4pter-4qter

Query Match 96.4%; Score 4026; DB 2; Length 820;

Best Local Similarity 96.9%; Pred. No. 2.8e-308;

Matches 776; Conservative 1; Mismatches 10; Indels 14; Gaps 4;

QY	3	ASSDPYLPYDGG-----DNIPRLRLKRGHTYMTNGSINSSTHLLDLDEPT 52
DB	22	ASSDEEL-LDGAIVINDFOPTSEDDNL-LDGDVAVGHYMTNGSINSSTHLLDLDEPT 79
QY	53	PGVGTVDDEFTIMVREKCKDRHRIRNSKKESAMEMTKSLYDAMSGLVYTLGLAS 112
DB	80	PGVGTVDDEFTIMVREKCKDRHRIRNSKKESAMEMTKSLYDAMSGLVYTLGLAS 139
QY	113	GALAGLIDIAADMTDKESICISALWYNHQQCWGNSNETTFEERDKCPQWKTAELIIG 172
DB	140	GALAGLIDIAADMTDKESICISALWYNHQQCWGNSNETTFEERDKCPQWKTAELIIG 199
QY	173	QAQPGSYIMNYIMYFWALSFAPLAVSVKVPAPACGSGEPEIKTITISGFTIRGLCK 232
DB	200	QAQPGSYIMNYIMYFWALSFAPLAVSVKVPAPACGSGEPEIKTITISGFTIRGLCK 259
QY	233	WTLMIKTITLVAVASGLSGKEGPLVHVACCGNIFSYLFPKYSTNEAKKREVLASA 292
DB	260	WTLMIKTITLVAVASGLSGKEGPLVHVACCGNIFSYLFPKYSTNEAKKREVLASA 319
QY	293	AGYSVAFGAPIGVLFSLSEVSYTFPLKTLMSRFAPALVAAPVLRISINPGNSRLVLPYV 352

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Db 320 AGVSAAGAPIGVGLFLEEVSYYPEKTLMRSPFAALVAAFLRSINPFGNSRLVLEYV 379
OY 353 EYHFWPLFELFEPILLGVFGGLGAFETIRANIAMCRKRSTKFGKPVLEVIIVAAITA 412
Db 380 EYHFWPLFELFEPILLGVFGGLGAFETIRANIAMCRKRSTKFGKPVLEVIIVAAITA 439
OY 413 VIAFPNPTRLNTSELIKELFTDCGPLESSSLCDYRNDMNAKIVDDIPDRPACIGVYSA 472
Db 440 VIAFPNPTRLNTSELIKELFTDCGPLESSSLCDYRNDMNAKIVDDIPDRPACIGVYSA 499
OY 473 IMWLCLALIFETITVTTFPGIKVPSGLFIPSMAGATAGRVYGAIVQOLAYHHNDWFLFK 532
Db 500 IMWLCLALIFETITVTTFPGIKVPSGLFIPSMAGATAGRVYGAIVQOLAYHHNDWFLFK 559
OY 533 EMCVAGADCTIPGLYAAVGAACGAGTGMTVSLVIVFELTGLLEYIVPLMAAVMTSKW 592
Db 560 EMCVAGADCTIPGLYAAVGAACGAGTGMTVSLVIVFELTGLLEYIVPLMAAVMTSKW 619
OY 593 VGDAFREGIYEAHIRLNGYFELDAAKE--EFTHTTLADAVMRPRNDPPLAVLTQDNMTV 650
Db 620 VGDAFREGIYEAHIRLNGYFELDAAKEEBEFTHTTLADAVMRPRNDPPLAVLTQDNMTV 679
OY 651 DDIEINMINETSYNGFPVIMSKESQRLVGFALRDLTIAIESARKKQEGIVSSRYCEAQH 710
Db 680 DDIEINMINETSYNGFPVIMSKESQRLVGFALRDLTIAIESARKKQEGIVSSRYCEAQH 739
OY 711 TPSPAESPRPLKRLSLDMSPTVTDHTPMEIYVDIFRKLGRLQCLVTHNGRLGIIITK 770
Db 740 TPSPAESPRPLKRLSLDMSPTVTDHTPMEIYVDIFRKLGRLQCLVTHNGRLGIIITK 799
OY 771 KDILRHMAQTANODPASIMEN 791
Db 800 KDILRHMAQTANODPASIMEN 820

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RESULT 2

S53473
chloride channel 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C:Accession: I48295; S53473
R:Borsani, G.; Ruggeri, E.T.; Tagliatalela, M.; Wong, C.; Ballabio, A.
Genomics 27, 131-141, 1995
A:Title: Characterization of a human and murine gene (CLCN3) sharing similarities to vol
A:Reference number: A57067; MUID:95394449; PMID:7665160
A:Accession: I48295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-760 <RES>
A:Cross-references: EMBL:X78874; NID:9854275; PIDN:CAA5476.1; PID:9854276
C:Genetics:
A:Gene: CLCN3

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Query Match 95.7%; Score 3996; DB 2; Length 760;
Best Local Similarity 99.7%; Pred. No. 5,7e-306;
Matches 736; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 32 MTNGSINSSTHLLDLDDEPIPGVGYDDFHTIDMVEKCKDRRHRIRNSKKKESAMEM 91
Db 1 MTNGSINSSTHLLDLDDEPIPGVGYDDFHTIDMVEKCKDRRHRIRNSKKKESAMEM 60
OY 92 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMPTDLKEGICLSALMYNHQCCWGSNE 151
Db 61 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMPTDLKEGICLSALMYNHQCCWGSNE 120
OY 152 TTFEERKCKPQWKMAELIIIGQABGPGSYIMNYIMYIFMALSFAPLAVSLVKYFAPYACG 211
Db 121 TTFEERKCKPQWKMAELIIIGQABGPGSYIMNYIMYIFMALSFAPLAVSLVKYFAPYACG 180
OY 212 SGPEIKTIIISGFIIRGYLCKWMLMTITTLVLAVASGLSLGKRGPLVHVACCCGNIFY 271
Db 181 SGPEIKTIIISGFIIRGYLCKWMLMTITTLVLAVASGLSLGKRGPLVHVACCCGNIFY 240

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OY 272 LFPKYSTNEAKKREVLSAASAGVSAFAPIGGVLEESLEEVSYYPEKTLMRSPFAALV 331
Db 241 LFPKYSTNEAKKREVLSAASAGVSAFAPIGGVLEESLEEVSYYPEKTLMRSPFAALV 300
OY 332 AAFVLRSTINPFGNSRLVLFVEYHTPWYLFELLFPIILGVFGGLGAFETIRANIAMCRRR 391
Db 301 AAFVLRSTINPFGNSRLVLFVEYHTPWYLFELLFPIILGVFGGLGAFETIRANIAMCRRR 360
OY 392 KSTFGKYPVLEVIIVAAITAVIAFNPYTRNLNTSELIKELFTDCGPLESSSLCDYRNDM 451
Db 361 KSTFGKYPVLEVIIVAAITAVIAFNPYTRNLNTSELIKELFTDCGPLESSSLCDYRNDM 420
OY 452 NASKIVDDIPDRPACIGVYSAIMQLALIFKIIIMVTFEGIKVPSGLFIPMAIGAIA 511
Db 421 NASKIVDDIPDRPACIGVYSAIMQLALIFKIIIMVTFEGIKVPSGLFIPMAIGAIA 480
OY 512 RIVGIAVEQLAYYHHDMFIFREKCEVAGADCTPGLYAAVGAACGAGTGMTVSLVIVF 571
Db 481 RIVGIAVEQLAYYHHDMFIFREKCEVAGADCTPGLYAAVGAACGAGTGMTVSLVIVF 540
OY 572 ELTGLLEYIVPLMAAVMTSKWVGDAFREGIYEAHIRLNGYFELDAAKEEFTHTTLADVM 631
Db 541 ELTGLLEYIVPLMAAVMTSKWVGDAFREGIYEAHIRLNGYFELDAAKEEFTHTTLADVM 600
OY 632 RPRNDPPLAVLTQDNMTVDDIENMINETSYNGFPVIMSKESQRLVGFALRDLTIAIES 691
Db 601 RPRNDPPLAVLTQDNMTVDDIENMINETSYNGFPVIMSKESQRLVGFALRDLTIAIES 660
OY 692 ARKQEGIVGSSRYCFQNHPTSLPAPESPRPLKRLSLDMSPTVTDHTPMEIYVDIFRKL 751
Db 661 ARKQEGIVGSSRYCFQNHPTSLPAPESPRPLKRLSLDMSPTVTDHTPMEIYVDIFRKL 720
OY 752 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 791
Db 721 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 760

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RESULT 3

I58159
protein kinase C-regulated chloride channel - black rat
C:Species: Rattus rattus (black rat, roof rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58159
R:Kawasaki, M.; Uchida, S.; Monkawa, T.; Miyawaki, A.; Mikoshiba, K.; Marumo, F.; Sas
Neuron 12, 597-604, 1994
A:Title: Cloning and expression of a protein kinase C-regulated chloride channel abun
A:Reference number: I58159; MUID:94206538; PMID:8155321
A:Accession: I58159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-760 <RES>
A:Cross-references: GB:D17521; NID:9473727; PIDN:BA04471.1; PID:9699624
C:Genetics:
A:Gene: CLC-3

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Query Match 95.6%; Score 3994; DB 2; Length 760;
Best Local Similarity 99.5%; Pred. No. 8,2e-306;
Matches 756; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 32 MTNGSINSSTHLLDLDDEPIPGVGYDDFHTIDMVEKCKDRRHRIRNSKKKESAMEM 91
Db 1 MTNGSINSSTHLLDLDDEPIPGVGYDDFHTIDMVEKCKDRRHRIRNSKKKESAMEM 60
OY 92 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMPTDLKEGICLSALMYNHQCCWGSNE 151
Db 61 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMPTDLKEGICLSALMYNHQCCWGSNE 120
OY 152 TTFEERKCKPQWKMAELIIIGQABGPGSYIMNYIMYIFMALSFAPLAVSLVKYFAPYACG 211
Db 121 TTFEERKCKPQWKMAELIIIGQABGPGSYIMNYIMYIFMALSFAPLAVSLVKYFAPYACG 180
OY 212 SGPEIKTIIISGFIIRGYLCKWMLMTITTLVLAVASGLSLGKRGPLVHVACCCGNIFY 271
Db 181 SGPEIKTIIISGFIIRGYLCKWMLMTITTLVLAVASGLSLGKRGPLVHVACCCGNIFY 240

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Db	121	TTEDROCKCPLMÖKMSSELLVNÖSEASVYILNLYMILMALLPFLANVSLVRVAPYRCG	180
QY	212	SGIPEIKTILSGFIIRGYLGRWPLMKITITVLVAVSLSGKEGRLVHVAOCGGNIPSY	271
Db	181	SGIPEIKTILSGFIIRGYLGRWPLMKITITVLVAVSLSGKEGRLVHVAOCGGNIPSY	240
QY	272	LEPKSTMEAKKREYLSAASAGSVANFAGIIGVLSLEEVSYFFPLKIMRSFPAALY	331
Db	241	LEFSKISKEGRRREYLSAASAGSVANFAGIIGVLSLEEVSYFFPLKIMRSFPAALY	300
QY	332	AAFLVRSINPFGNSRLVFEYVEHTPWLFLEFPILLGLVGGVLMGAFIPANIAMCRR	391
Db	301	AAFLVRSINPFGNSRLVFEYVEHTPWLFLEFPILLGLVGGVLMGAFIPANIAMCRR	360
QY	392	KSTRGKYPVLEVIIVAAIIVAFPNPYTRLNTSELIKELFTDOCPLESSLCDYRDM	451
Db	361	KTRLRGKYPVLEVIIVAAIIVAFPNPYTRLNTSELIKELFTDOCPLESSLCDYRDM	420
QY	452	NASKYVDIPRRPAGIIGVYSALWOLCALIFKIMTYVTFSGIRKYPSCGLFIPMAIGATG	511
Db	421	NMTREVDDIPRRPAGIIGVYSALWOLCALIFKIMTYVTFSGIRKYPSCGLFIPMAIGATG	480
QY	512	RIVGIAVQOLVYHHDMIFKEMCEVGDCTTGGIYAVVGAACAGGTMTVSJVIYVE	571
Db	481	RIVGIAVQOLVYHHDMIFKEMCEVGDCTTGGIYAVVGAACAGGTMTVSJVIYVE	540
QY	572	ELTGLEIYVPLMAAVMTSKWVGDAFNGREGIYEAHIRLNGYPLFDAAEEFTHTVLADVM	631
Db	541	ELTGLEIYVPLMAAVMTSKWVGDAFNGREGIYEAHIRLNGYPLFDAAEEFTHTVLADVM	600
QY	632	RRRRNDPPLAVLTQDNMTVDIENKINETSNGRPVIMSKESQRLVGFALRRDLTIAES	691
Db	601	RRRRNDPPLAVLTQDNMTVDIENKINETSNGRPVIMSKESQRLVGFALRRDLTIAES	660
QY	692	ARKKOEGIVGSSRPFCAHPHPSLPAESRPLKLSILDMSPFYTHDPMRIYVDIRKL	751
Db	661	ARKKOEGIVGSSRPFCAHPHPSLPAESRPLKLSILDMSPFYTHDPMRIYVDIRKL	720
QY	752	GIROCLVTHNGRLLGIITRKDILRHMAQTADQASIMFN	791
Db	721	GIROCLVTHNGRLLGIITRKDILRHMAQTADQASIMFN	760
RESULT 5			
chloride channel protein 3 - rat			
S47327			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999			
C:Accession: S47327			
R:Schwappach, B.; Jentsch, T.J.			
submitted to the EMBL data library, September 1994			
A:Reference number: S47327			
A:Accession: S47327			
A:Status: Preliminary			
A:Molecule type: mRNA			
A:Residues: 1-747 <SCH>			
A:Cross-references: EMBL:Z36944; NID:g535931; PIDN:CA85406.1; PID:g535932			
Query Match			
Best Local Similarity 77.6%; Score 3240; DB 2; Length 747;			
Matches 586; Conservative 81; Mismatches 80; Indels 0; Gaps 0;			
QY	45	LDLLEDEPIPGCVTDDPFTIDMWREKCKDPRHRIRISKKKESAMWMTKSLYDAGSGMLV	104
Db	1	MDFLDEPRPDVGYTEDHTIDMLREKSRDIDRHKIKTSKESIMWFKSLDAGSGMLV	60
QY	105	VTLTGASLGLIDIAADMTDLKGLGICLSALMYNHEDOCWGSNETFEEDRDCPOMK	164
Db	61	MLTIGLLAGTLAGVIDLAVDMTDLKGGVCLASAFWYSHEDCCWTSNETFEEDRDCPOMK	120
QY	165	TWALIIIGQAGPGSGSYIMNYIMYFALSAFPLAVSLVKYFAPACSGIPEIKTILSGF	224
Db	121	KWSELILQSQSGAASVAILNLYIMLALFALFVLSVVRFAFAPACSGSGIPEIKTILSGF	180

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QY 225 IIRGYLKWTLIMITITVLAVASGLSLGKRGPLVHVACCGNIFSLPKYSTNEAKR 284
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 IIRGYLKWTLIMITITVLAVASGLSLGKRGPLVHVACCGNIFSLPKYSTNEAKR 240
QY 285 EVLSAASAGVAVFAGPARGVLSLEEVSYFPLKTLMSFFALVAALVLRISINFGN 344
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 EVLSAASAGVAVFAGPARGVLSLEEVSYFPLKTLMSFFALVAALVLRISINFGN 300
QY 345 SRLVLFVEYHTPPYMAELPEFILLGVGGLMGVTFRCNIAACRRKRTKRGYPVLEV 404
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SRLVLFVEYHTPPYMAELPEFILLGVGGLMGVTFRCNIAACRRKRTKRGYPVLEV 360
QY 405 IIVAAITAVIAFPNRYRLNTSELILKELFTDCCPLESSLCDYRNDNASKIYDIDR 464
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 IIVAAITAVIAFPNRYRLNTSELILKELFTDCCPLESSLCDYRNDNASKIYDIDR 420
QY 465 AGIVSAIMQCLALIFKIIIMVFTGIVKPSGLFIPSAIGAIAIGVIAVEQLAY 524
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 AGIVSAIMQCLALIFKIIIMVFTGIVKPSGLFIPSAIGAIAIGVIAVEQLAY 480
QY 525 HHDFIKREKCEVAGADCITTEGLYAMVGAACLGVTMTVSLVYIVELTGLGYIPLM 584
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 HHDFIKREKCEVAGADCITTEGLYAMVGAACLGVTMTVSLVYIVELTGLGYIPLM 540
QY 585 AAATSKWVDAFREGIEYEAHRLNGYPLDLAKEEFTHTTADVNRPRRNDPLAVLT 644
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 AAATSKWVDAFREGIEYEAHRLNGYPLDLAKEEFTHTTADVNRPRRNDPLAVLT 600
QY 645 QDNMTVDIEMINETSNGFPVIMSKESORLVGFALRDLTIAIESARKKOEIVGSSR 704
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 QDSMTVEDVETLKEITDNGFPVIMSKESORLVGFALRDLTIAIESARKKOEIVGSSR 660
QY 705 VCFAGHTPSLPASPRDLKRLSLDMSPTVTDTHTPMEIYDIFRKLGRLCTHTNGRL 764
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 MYTEEPPELPANSPHRLKRLSLDMSPTVTDTHTPMEIYDIFRKLGRLCTHTNGRL 720
QY 765 LGITTKDILRHMAOTANODPASTMEN 791
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 LGITTKDILRHMAOTANODPASTMEN 747

RESULT 6
I48294
gene C1c4 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48294
R:Rugali, E.I.; Adler, D.A.; Borsani, G.; Tsuchiya, K.; Franco, B.; Hauge, X.; Distche
Nature Genet. 10, 466-471, 1995
A:Title: Different chromosomal localization of the C1c4 gene in Mus spretus and C57BL/6
A:Reference number: I48294, M0ID:95400329; PMID:7670496
A:Accession: I48294
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1747 <RES>
A:Cross-references: EMBL:249916; NID:929679; PIDN:CAA90150.1; PID:929680
C:Genetics:
A:Gene: C1c4

Query Match 77.0%; Score 3217; DB 2; Length 747;
Best Local Similarity 77.0%; Pred. No. 1e-244;
Matches 580; Conservative 83; Mismatches 84; Indels 0; Gaps 0;

QY 45 LDLDDEPIPVGYDDEFTIDWVEKCKDRERHRIRNSKKESAMWTKSLYDAMSGMLV 104
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDLFEPEFPDVGTEDEHTIDWVEKCKDRERHRIRNSKKESAMWTKSLYDAMSGMLV 60
QY 105 VTLTGLASGALGLIDIAADMTDLKEGICLSALWVHEOCWGSNETFEEDRCPQMK 164
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MLTIGLAGTLAGYIDIAADMTDLKEGVCLSAFWYSHEOCWGSNETFEEDRCPQMK 120
QY 165 TMAELLIGQAGEGPSYIMNTIMYFMAISFAFLAVSLVKKVAPACSGSIPETITLSGF 224

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Db 121 KMSLELLSQSEAGASAYILNMYLTMALFPAFLAVSLVRFAPACSGSIPETITLSGF 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 225 IIRGYLKWTLIMITITVLAVASGLSLGKRGPLVHVACCGNIFSLPKYSTNEAKR 284
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 IIRGYLKWTLIMITITVLAVASGLSLGKRGPLVHVACCGNIFSLPKYSTNEAKR 240
QY 285 EVLSAASAGVAVFAGPARGVLSLEEVSYFPLKTLMSFFALVAALVLRISINFGN 344
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 EVLSAASAGVAVFAGPARGVLSLEEVSYFPLKTLMSFFALVAALVLRISINFGN 300
QY 345 SRLVLFVEYHTPPYMAELPEFILLGVGGLMGVTFRCNIAACRRKRTKRGYPVLEV 404
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SRLVLFVEYHTPPYMAELPEFILLGVGGLMGVTFRCNIAACRRKRTKRGYPVLEV 360
QY 405 IIVAAITAVIAFPNRYRLNTSELILKELFTDCCPLESSLCDYRNDNASKIYDIDR 464
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 IIVAAITAVIAFPNRYRLNTSELILKELFTDCCPLESSLCDYRNDNASKIYDIDR 420
QY 465 AGIVSAIMQCLALIFKIIIMVFTGIVKPSGLFIPSAIGAIAIGVIAVEQLAY 524
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 AGIVSAIMQCLALIFKIIIMVFTGIVKPSGLFIPSAIGAIAIGVIAVEQLAY 480
QY 525 HHDFIKREKCEVAGADCITTEGLYAMVGAACLGVTMTVSLVYIVELTGLGYIPLM 584
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 HHDFIKREKCEVAGADCITTEGLYAMVGAACLGVTMTVSLVYIVELTGLGYIPLM 540
QY 585 AAATSKWVDAFREGIEYEAHRLNGYPLDLAKEEFTHTTADVNRPRRNDPLAVLT 644
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 AAATSKWVDAFREGIEYEAHRLNGYPLDLAKEEFTHTTADVNRPRRNDPLAVLT 600
QY 645 QDNMTVDIEMINETSNGFPVIMSKESORLVGFALRDLTIAIESARKKOEIVGSSR 704
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 QDSMTVEDVETLKEITDNGFPVIMSKESORLVGFALRDLTIAIESARKKOEIVGSSR 660
QY 705 VCFAGHTPSLPASPRDLKRLSLDMSPTVTDTHTPMEIYDIFRKLGRLCTHTNGRL 764
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 MYTEEPPELPANSPHRLKRLSLDMSPTVTDTHTPMEIYDIFRKLGRLCTHTNGRL 720
QY 765 LGITTKDILRHMAOTANODPASTMEN 791
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 LGITTKDILRHMAOTANODPASTMEN 747

RESULT 7
T19065
probable protein kinase C-regulated chloride channel C07H4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19065; T25256
R:Percy, C.
submitted to the EMBL Data Library, January 1996
A:Reference number: T19065
A:Accession: T19065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-735 <MIL>
A:Cross-references: EMBL:268334; PIDN:CAA92728.1; GSPDB:GN00020; CESP:C07H4.2
A:Experimental source: clone C07H4
R:lighting, J.
submitted to the EMBL Data Library, September 1995
A:Reference number: T20005
A:Accession: T25256
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-735 <MIL>
A:Cross-references: EMBL:254216; PIDN:CAA90349.1; GSPDB:GN00020; CESP:C07H4.2
A:Experimental source: clone T24H10
C:Genetics:
A:Gene: CESP:C07H4.2
A:Map position: 2
A:Insertions: 35/2; 81/3; 242/3; 297/3; 337/2; 537/3; 634/2; 682/3

```

Query Match 50.3%; Score 2100.5; Db 2; Length 735;
Best Local Similarity 53.4%; Pred. No. 6.2e-157;
Matches 404; Conservative 121; Mismatches 181; Indels 51; Gaps 9;

```
QY      PGVGVYDDPHITDWVRKCKDREHRRIRINSKKRESAMEMTSLYDAMSGMLVTLTGLAS 112
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 PPFKSYGDFPHITDWQRDLARDRLRIKRIKSKKVPDPPLGLSGMDAGAGWICVLEFVGAA 63

QY      113 GALAGLIDIAADWMTDLKEGICLSALWYNHDDCCGSGNETTEFHEHDKCPQWKTAAELIG 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 GATAGIIDIIGARWMSDLKTGYCADRFWLDHEHCWSSNDTFKQ--DDCKAMTKMPMML-- 120

QY      173 QAEGGSIT---MNTIMIFNALSFAPLAVSLVKFAFAPACSGIPEKTIISGTTIRGY 229
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 NYNSSSFLFLEWIEFPIGAVAMSTLAVLFVKITFAFACGSGIPEKTIISGTVIRGY 180

QY      230 LCKWTLMTKTTTLVLAVNSGLSGKEGFLVHVACCGCNFSTLFPKYSTNEAKKREVLSA 289
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 LCKWTFITKSGVLLISSAGSLSGKEGPMVHLACICGINFTSLFPKYLNEKKKEITLSA 240

QY      290 ASAGVSAVAFGAPLIGVLFSLEENSVYRPLKTLWRSFPAALVAFAVLRSINPFNSRLVL 349
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 SAAGVSAVAFGAPIGVLFSLSEASVYRPLKTLWRSFPCALVACILFVAPNFGSNQSL 300

QY      350 FYVEHTHWLYLELEPPILLGVGGLKCAFFIRANIAMCRKRSKTK-FGKIPVLEVIIVA 408
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301 FHVDTMMKTFLELVPFALILGFLGILSLFFANIRMSRFKNSKMGNDPIYEVMLIT 360

QY      409 AITAVIARPNPTRLNLTSELIKELFTDC-GPLESSSLCDYRNDMAKSIYVDIPDPAGI 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      361 LVTAALISTFNPTKRSQAQSMIQQLFRCEDQIDEDSLCDQNKALSI----- 406

QY      468 GYSAIMOLCLALFKIIMTFTEFGIKVPSGLFIPSMAGIACIRVIGAEQL----- 521
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      407 ----AFQGLLMALIFKFIYITTFEGIKVPCGLFVPSISGMAGILGITYDQITRAVQA 462

QY      522 AYVHHDFIEKMECEVGADCTTGPLYANVGAACIGVTRMTVSLVIVFELTGLGLEYIV 581
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      463 TPGHSDYFT----CQIGKDCVMPGLYAVGAAVILGVTBMTVSLVIMFELTGLSEFTIV 518

QY      582 PLMAVMTSKVWGOAFGREGIYEAHIRLNGYRFLDKAKEEFTHTTLAADVMR----- 633
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      519 PLMAVMTSKMIGDISMGIYEAHIELNGYRFLDSKGEYRSTVYASQVMRSIHRQVAD 578

QY      634 -----RRNDPPLAVLTQDNMTVDVDIENMNETSVNFPYIMSKESQRLVGFALRPDLT 686
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      579 EMSMDRELKLNELSVITESGMTLGDLESLLRQIDFNKFPVYVSSNMHLVGFITRRDIL 638

QY      687 IALISARRKQSGIVGSSRYNCFQAQHTPSSLPAESPRDLKRLSILDSMPTVTDTHTPMEIYVD 746
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      639 IALHTARKTQPVVYVNSIAYFSDDGVPDAMPGPAPRLRLKILIDMAPMTVDTQTMEETVID 698

QY      747 IFRKGLGQCLVTHNNGRLGIIITKKDILRHMAQIRANQ 783
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      699 MFRKGLRHLVLTKNKGLGIITKKDILQFMKNNKNSQ 735
```

RESULT 8
137277
C:chloride channel protein, kidney - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I37277
R:Flisher, S.E.; Black, G.C.; Lloyd, S.E.; Hatchwell, E.; Wrong, O.; Thakker, R.V.; Craig
A:Title: Isolation and partial characterization of a chloride channel gene which is expr
A:Reference number: I37277; MUID:95179126; PMID:1874126
A:Accession: I37277
A:Status: preliminary; translated from GR/EMBL/DBU
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: EMBL:X81836, NID:9577052, PIDN:CAA57430.1; PID:9577053
A:Genetics:

A:Gene: GDB:NPHL2; DENTS
A:Cross-references: GDB:433706; OMIM:300009
A:Map position: Xp11.23-Xp11.22
A>Note: defects in this gene may cause nephrolithiasis 2, x-linked Dent disease

Query Match 26.0%; Score 1086; DB 2; Length 260;
Best Local Similarity 79.1%; Pred. No. 9.5e-78;
Matches 204; Conservative 29; Mismatches 25; Indels 0; Gaps 0;

OY 534 WCEVADICITRLPLVMGAACAGCGVTMTNVLIVYVEFELTGLLEYIPLMAAVTSKV 593
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 WCSQADDCITRELYAMVGAAACGCVTRMYSLIVIMEFLIGLEFYIPLMAAATSKV 62
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 554 GDAPREGCIYEAHIRLNLNGYPRDLAKEEFTHTTLAADVRRPARRNDPLAVLTQDNMTVDI 653
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 ADALRGEGYDHRHILRNLGYPRPLEAKEEPFAHKRTLAMDVKRPARNPDILTTLTQDSMTVEDV 122
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 654 EMMINETSNGFPVYMSESRQLVGFALRDLLTAIEASARKKQBGIVSSKVCRAQHPS 713
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 ETIISETTYSGFPVVARSEROLVGEFLRDLIIISIAENAKKKOOGVSTSIIFYTEHSPP 182
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 714 LPAESPRPLKLRSIDMSPPFYTDDTPMEIWDIPRKLGLOCLVTNHGRLLGIITTKDI 773
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 LPPYTPPLKLRLNIIDLSPFTYTDLPMEIYVDIPFKLGLOCLVTNHGRLLGIITTKDV 242
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 774 LRHMAOTANODPASIMFN 791
 | : : | | | | | | | : : | | | | | | : : | | | | | | : : | |
Db 243 LKHINOMANOOPDISLFN 260
 | : : | | | | | | | : : | | | | | | : : | | | | | | : : | |

RESULT 9
T02805
chloride channel protein CCP [imported] - Leishmania major (strain Friedlin)
C.Species: leishmania major
C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C.Accession: AB1457; T02805
R.Miyler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A.Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein
A.Reference number: AB1455; MUID:99178987; PMID:10077609
A.Accession: AB1457
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-772 <Pyl>
A.Cross-references: GB:A0001274; NID:93264850; PIDN:AAC24628.1; PID:g2995581; GSPDB:G
A.Experimental source: strain MHOM/Lt/81/Friedlin
C.Genetics:
A:Gene: CCP
A:Map position: 1

Query Match 24.4%; Score 1020.5; DB 2; Length 772;
Best Local Similarity 32.0%; Pred. No. 5.5e-72;
Matches 240; Conservative 140; Mismatches 314; Indels 57; Gaps 14;

OY 36 GSINSSTHLILLDEPIGVGTYPDFFHTIDWVRCKDKDERHRIRINSKKESAWEMTKSL 95
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 GADESITMLVVNVSA-----DMATIDCIRSITEAE---RAAMWRRRSARATAASSS 73
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 96 Y-DAMS-----GMVVTTLTGLASGALGLIDLAADMMDLKGGICLSALMVHHQQCW 147
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 74 YGDKWVSYPSEGEEAFMAACGIVLCIGVFSDCAHWVASFRSGICANFMFLGRNNKC 133
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 148 GSNETTFEEROKCPQMKWAELLIGQEGPSSYLNNYIMYIFMALSFATLAVSLVKYFAP 207
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 DCRE-----CGEYSWGFEFLGRDNHVAAFY-DIPMNYFSFTMAAYTAAYLCTKYAP 184
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 208 YACGSGIPEIKTIISGFIIRGLYTKWTLMITITLVLAVASGLGKEGPVLVHAACCGN 267
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 185 YASGGIAEVKTIYSGHHVKRYLDGWLITIKVYGMCSTSGGLTVGKEGPPVTHIGACYGC 244
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 268 IFSYLEPKYSTNEAKKRREVLSAASAGVSAFGAPIGGVLFLEEVSYYEPPLKTLMRSPF 327
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 245 IISGALPFYO-QEKKERLITAGAGGMAVAFGAPVGGVIFALDVSYSTYFKALMALI 303
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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OY 328 AALVAAPVLSINFGSRLVLYVEVHEHPMYLFELEPFLLGVCGLMAFEPILANIM 387
Db 304 CGVAVVLLOSVDIMHTGRIVOFESVYNQHNHMFELPMFAIGCFGFMGSTFSVNLHV 363
OY 388 CRRRSKTRKFGKRYPLEVILVAITAVIAEPNPYTRLNTSELIKELFTDGPLESSLCDY 447
Db 364 GRWRKK-HLRQWRIVEVAVAATGVVNFLETPYGGSMLELGDFOCTPGSTMEME- 421
OY 448 RNDMAASKYDDIDFDRAGAGVCSALMOCLALIEFIINTVTFPGIKVPSGLIFISMAIG 507
Db 422 DSDLR-----AFSLLVATAFAEFAATVGFPLAGILVPSLTIG 462
OY 508 AIAIRIGIAVEOLAYHHMDIEFKEMCEYAGDCILPGIYAUGAAACIGVTRMTYSLV 567
Db 463 ALYGRAGMFMRAIOETIYASSIYFTE-CYDQDCLVIPGYVALVGAAMLMGTHTMIELA 521
OY 568 VIVFELTGLEIYVPLMAAVMTSKWGDAPGREGIYEAHIRLNGYFELDAKEEPTHTTLA 627
Db 522 IIMFELTGSLEYWVPVIVGILCAKAGAEGAVGKGTGEIIEENKRLPYLDPPKKEFLDEVA 581
OY 628 ADVWRPRNDPLAVLVLQDMWTDJLENNIMNETSYGPFVIMKSESORJUYGALRDRDTI 687
Db 582 KDYV-----GNKQFVLTAYGLQVRDINELYTKKNVYGFVYVESLSDVYLLGLAPPKYVR 637
OY 688 AIESARRKQEGIVGSSNVCFAOHTPSLPAESP-RPLKRSILDMSPFVYTDHTPMEIYVD 746
Db 638 ALOVAAARNSDMNLNTYIRE-KTKPSHSRPAFLEVDLIGLIESCLLOVEPECVYKCKLLY 696
OY 747 IFRLLGRQCLVTHNGRLGLIIRKILIRHM 777
Db 697 LFKSLGTHTHTFYCYSKFEBCFISKDPFINFM 727

```

hypothetical protein SPBC19C7.11 - fission yeast (*Schizosaccharomyces pombe*)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39817
R:Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Lucas, M.; Gallardin, C.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21881
A:Accession: T39817
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-812 <LTYN>
A:Cross-references: EMBL:AL023859, PIDN:CAI19579.1; GSPDB:GN00067; SPDB:SPBC19C7.11
A:Experimental source: strain 972h-; cosmid c19C7
C:Genetics:
A:Gene: SPDB:SPBC19C7.11
.:Map position: 2

Query Match	24.3%	Score 1015	DB 2	Length 812
Best Local Similarity	32.0%	Pred. No. 1.6e-71		
Matches 240	Conservative 142	Mismatches 275	Indels 94	Gaps 17

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Oy 72 KDRKRRHRINRKKKE-----SAMEMTKSLVDAMSGWLVVLTGLASALGLGDIADMM 126
Db 64 KDRV-NEIINONEBNVDIOSRMSKLMRIMVNGISWTLISLTIGTWGFAAYMIDYTSWL 122
Oy 127 TDLKEGICLSALWYNHEOCCWGS-----NEFTFEERDKCPOMKTWAEIIQOAE 175
Db 123 SDIRGTCYTSIMHYINERKCCCYSETMGMEFKHLDYNDLTF-QGSSCTAMKRWY----- 174
Oy 176 GPGSYIMWYIMFWALSFAPLAVSLVKVPAPYAGSGDEIKTILSGTIRGLGKWL 235
Db 175 ---KRSYNYLLYTFALLFVLCALIMVDVAPLAAAGSGEIKCIIISGFLRDSFLSFRVM 231
Oy 232 MIKTTITVLAAASGSLGKEBGLVHVAACCGNIFSYLFPKYSTNNAKKREVLNAAAGV 235
Db 232 LVKCGGLPLAASGLSVGKEBSPYHLATTTIGHNISKIFKYARREGSINYRQIVAAASGV 231

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0Y 296 VAAFCAPJGVLGVEFSE-----EVSYPELKTMRSEFALVAALVLRSNPE 342
Db 292 AABESPSJGVLFGLEVAKFIEILNFKEMSGVDPRMIVYSFCCLSANGVLHMLNPF 351
0Y 343 GNSRLVLFVEYHHWPVYFELPEPILLGVBCGLGAPFIRANIAMCRRRSTKFGKYPVL 402
Db 352 RTGQVLFEEVRRSGSMHFELLFCFCLGFGVLGFEFMRLEPFIOLKRRK-YLSRNVL 410
0Y 403 EVIIAATTAIVAPNPVTRLNTESELKEFLPDGCEPSSS-----LCQVRNDMASKI 456
Db 411 DAAPVTVTTSLSFLNPLMRIDMTLGMELLFOEC---KSSSPELINLCO----- 457
0Y 457 VDDIPDRPAGIVYSALWQLCLALFKITIMVFTFGIKVPSGLEIFPSMAIGLAGRIVGI 516
Db 458 -----PSLRKNTI-LLLIATFARTIEVTFYSGAKVPAGIVPSMAGASGFYIGL 508
0Y 517 AVEQLAYHHBMFIFKMECEYGCADCIIPGLAAMGAACLOGVARMVSLVIVYFELTGG 576
Db 509 IAEIMYQRFPNYSVLELA-CHGSESCITPFGYIALLGAALASGLIMHLVTVIIVFELTGA 567
0Y 577 LEYIVPLMAAVTSKWVGDAFGRGIVYEAHTRLNGVYFLDAKEEFTHTTLAADVMPRRN 636
Db 568 LNFIFPLVALVALANSIGNMLGKTGIADRSIEIGNDPLPEKEINSNTI-----N 619
0Y 637 DPLPLVLPQDMNVDDIE-----NMINETSNGVFPYIMKESQRLVGFALBRDLTAI 689
Db 620 IPTEVMAASNLITPSIGFTFRKLKLGMEGYDGSYIVLSDRSNYIILGYLKSSLSSSF 679
0Y 690 ESARKKQEGIVGSSHVCEAQ-----HTPSLPAESPRDLKURLSLIDMSPEFTVDHTMEI 743
Db 680 EAA-KLEESFTFDQOLCGKVDVSGDKSSKSFGESEDR-IDLSAYMDVNPISVLHTOSIAN 737
0Y 744 VVDIFRKGLQOCLVTHNGSLRGITTKDIL 774
Db 738 VAVLEFVLSPVIFIEKDGNLVGLSKDIL 768

```

RESULT 11
S50054
chloride channel protein CLC-1 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein GTC779; protein J1616; protein YJN040W; voltage-gated chlo
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1995
C:Accession: S50054; S39904; S57059; S63763
R:Huang, M.E.; Chuat, J.C.; Galibert, F.
J. Mol. Biol. 242: 595-598, 1994
A:Title: A voltage-gated chloride channel in the yeast Saccharomyces cerevisiae.
A:Reference number: S50054; MUID:95018225; PMID:7932715
A:Accession: S50054
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-779 <MAN>
A:CROSS-references: EMBL:L29347; NID:9576927; PIDN:AAA53399.1; PID:g576928
R:Greene, J.R.; Brown, N.H.; DiDomenico, B.J.; Kaplan, J.; Eide, D.J.
Mol. Gen. Genet. 241, 542-553, 1993
A:Title: The GFL1 gene of Saccharomyces cerevisiae encodes an integral membrane prote
A:Reference number: S39904; MUID:94088447; PMID:7505388
A:Accession: S39904
A:Molecule type: DNA
A:Residues: 1-12, R', 14-206, 'L', 208-256, 'T', 258-261, 'L', 263-496, 'I', 498-779 <GRE>
A:CROSS-references: EMBL:Z23117; NID:9619512; PIDN:CAA80663.1; PID:9435539
R:Huang, M.E.; Chuat, J.C.; Galibert, F.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57052
A:Accession: S57059
A:Molecule type: DNA
A:Residues: 1-779 <MAN>
A:CROSS-references: EMBL:Z49540; NID:91015690; PIDN:CAA89567.1; PID:91015691; MIPS:YJ
R:Huang, M.E.; Chuat, J.C.; Galibert, F.
Yeast 11, 775-781, 1995
A:Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes

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Db      629  EDKEEKEKRCIGYVLKRLHASKIMQSVNSTK---AQTLVYFNKSNEEL-GHRENCIGF 684

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Db 558 YAMTISLTAIMETKIDITFGLPIMLVLMVTKWVGDMF-NEGLEYDAHIDLAEPVILGNNP 616

Fri May 16 14:42:36 2003

us-09-804-472-2.rpr

Page 10

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Oy      720 R-----PLKRSILDM-----SPFYDHTPTMEIWDIPRL 751
          |         |         |         ||| : : : : : 
Db      771 RLSVAEMADYPRPDHDDLTLLNPRMIVDPVPMNSPFYTSPTHVSQFNLFRTM 820

Oy      752 GLRQC-LVTNGRCILGITKKDIIRHAAQ 779
          ||| : : : : : 
Db      831 GLRHLPVNANVGELGITRNINLYEFLQ 859
```

Search completed: May 12, 2003, 15:06:01
Job time : 54 secs